AMENDMENT

IN THE SPECIFICATION:

Please amend paragraph [0055] on page 21 of the specification as originally filed as follows:

-- DNA sequence variations, for example, DNA polymorphisms, at a restriction site relevant to the methods of the present invention may simulate DNA modification differences across individuals. Data from the SNP consortium ~~(ncbi.nlm.nih.gov/SNP)~~ indicate that roughly every 360th nucleotide in the human genome represents a SNP. In humans approximately 2.16 million SNPs are detectable in CpG dinucleotides, and such CpG SNPs are 6.7-fold more abundant than expected. See the NCBI Single Nucleotide Polymorphism website at ncbiDOTnlmDOTnihDOTgov/SNP, wherein "DOT" is ".". Depending on the restriction enzyme combination, CpG island array-based studies shown in FIG. 8 indicate that 10%/30% of all outliers that were originally detected as methylation differences contained SNPs. Information on the SNPs within the restriction sites of the enzymes used for the enrichment of the unmethylated or hypermethylated fractions is helpful in differentiating the epigenetic variations from the DNA sequence variations. --

Please amend paragraph [0108] on page 38 of the specification as originally filed as follows:

-- Since restriction enzymes are used in the enrichment of differentially modified DNA fractions, DNA sequence variation may simulate epigenetic differences. However, until now, microarray methods used in epigenetic studies have not been differentiating between methylation changes and the presence of SNPs within the restriction sites of the applied restriction enzymes. An approach for excluding the impact of DNA sequence variation, is to check the available SNP databases in order to identify the DNA sequence variation within the restriction sites of the used enzymes. For example, our 100 kb COMT array contains a total of 273 SNPs ~~(SNPper, http://snpper.chip.org/bio/snpper-enter)~~ out of which 101 (37%) reside within CpG dinucleotides and 55 (20%) SNPs are located within the restriction site of the four main enzymes, HpaII, Hin6I, AciI, and HpYCH4IV, which are used to interrogate the methylation patterns. See the SNPper

web-based tool available at snpperDOTchipDOTorg, wherein "DOT" is ".". The majority of these CpG-SNPs were located in AciI and HpaII restriction sites, whereas Hin6 and HpyCH4IV sites contained fewer polymorphisms (data not shown). --

Please amend the first paragraph on page 48 of the specification as originally filed as follows:

-- i) Oligonucleotides for microarrays. Using the publicly available human genome sequence of DRD2 plus wide upstream and downstream regions ~~(http://genome.ucsc.edu/)~~, 40-50 base oligonucleotides (with amino modifiers at the 5' end) that cover the testable genomic region of .about.350 kb are designed. See genomeDOTucscDOTedu, wherein "DOT" is ".". In epiG studies, sufficient coverage is achieved by about 3-5 (or more) oligonucleotides per kilobase of genomic DNA. Repetitive DNA elements maybe excluded using the RepeatMasker, which reduces the length of the target sequence from about 350 kb to about 200 kb. This requires about 800 oligonucleotides that will be synthesized for example, but not limited to at Qiagen, and then spotted on the glass at a specific location, for example, but not limited to the UHN Microarray Facility. --